

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/201,916

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/201,916DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Hope, Ralph Graham
 2 Mclaughlan, John
 3 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
 4 <130> FILE REFERENCE: DY0U17.001AUS
 5 <140> CURRENT APPLICATION NUMBER: US/09/201,916
 6 <141> CURRENT FILING DATE: 1998-12-01
 7 <160> NUMBER OF SEQ ID NOS: 13
 8 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 9 <210> SEQ ID NO 1
 10 <211> LENGTH: 630
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Hepatitis C Virus
 13 <220> FEATURE:
 14 <221> NAME/KEY: CDS
 15 <222> LOCATION: (43)...(630)
 16 <400> SEQUENCE: 1
 17 ggtgcttgcg agtgcccccgg gagggtctcg agaccgtgca cc atg agc acg aat 54
 18 Met Ser Thr Asn
 19 1
 20 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102
 21 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
 22 5 10 15 20
 23 gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150
 24 Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly Val Tyr Leu
 25 25 30 35
 26 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198
 27 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
 28 40 45 50
 29 tcc gag ccg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246
 30 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
 31 55 60 65
 32 cgt ccg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294
 33 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 34 70 75 80
 35 ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc 342
 36 Leu Tyr Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
 37 85 90 95 100
 38 agt ggc tct ccg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg 390
 39 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Ser
 40 105 110 115
 41 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat 438
 42 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
 43 120 125 130
 44 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc 486

Does Not Comply
Corrected Diskette Needed
PR 3-4

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Input Set: I201916.RAW

45 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
 46 135 140 145
 47 agg gcc ctg gcg cat ggc gtc cggtt ctg gaa gac ggt gtg aac tat 534
 48 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
 49 150 155 160
 50 gca aca ggt aac ctt cct ggt tgc tct ttc atc ttc ctt ctg gcc 582
 51 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
 52 165 170 175 180
 53 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac 630
 54 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
 55 185 190 195
 56 <210> SEQ ID NO 2
 57 <211> LENGTH: 60
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Hepatitis C Virus
 60 <220> FEATURE:
 61 <221> NAME/KEY: CDS
 62 <222> LOCATION: (1)...(60)
 63 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
 64 <400> SEQUENCE: 2
 65 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
 66 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
 67 1 5 10 15
 68 ggc gcc cct ctt 60
 69 Gly Ala Pro Leu
 70 20
 71 <210> SEQ ID NO 3
 72 <211> LENGTH: 18
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Hepatitis C Virus
 75 <220> FEATURE:
 76 <221> NAME/KEY: CDS
 77 <222> LOCATION: (1)...(18)
 78 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
 79 <400> SEQUENCE: 3
 80 ggt gtg aac tat gca aca 18
 81 Gly Val Asn Tyr Ala Thr
 82 1 5
 83 <210> SEQ ID NO 4
 84 <211> LENGTH: 1900
 85 <212> TYPE: DNA
 86 <213> ORGANISM: Human
 87 <400> SEQUENCE: 4
 88 cgtcttcggg aegcgccccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60
 89 gaagaaaaat ggcatccgtt gcagttgtatc cacaaccgag tgggtgtact cgggtggtca 120
 90 acctgcctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaagg 180
 91 accagtatcc ctacctgaag tctgtgtgt agatgscaga gaacgggtgtg aagaccatca 240
 92 cttccgtggc catgaccagt gctctgccc tcatccagaa gctagagccg caaattgcag 300
 93 ttgcccatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
 94 atcagccatc aactcagatt gttgcataatg ccaaaggcgc tgtgactggg gcaaaagatg 420

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RAW SEQUENCE LISTING
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W--> 95 ctgtgacgac tactgtgact gggccaagg attctgtngc cagcacgatc acaggggtga 480
 96 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagtg 540
 97 gcagcattaa cacagtctt gggagtcgga tgatcagct cgtgagcagt ggcgtagaaa 600
 98 atgcactcac caaatcagag ctgttggtag aacagtagct ccctctcact gaggaagaac 660
 99 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctgt tcagaagcca agttattatg 720
 100 ttagactggg atccctgtct accaagcttc actccctgca ctaccagcag gctctcagca 780
 101 gggtaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840
 102 acctgattga atttgcagg aagaatgtgt atagtgccaa tcagaaaatt caggatgctc 900
 103 aggataagct ctacctctca tggtagagt ggaaaaggag cattggatat gatgatactg 960
 104 atgagtccca ctgtgctgag cacattgagt cacgtactct tgcaattgcc cgcaacctga 1020
 105 ctcagcagct ccagaccacg tgccacaccc tcctgtccaa catccaaggt gtaccacaga 1080
 106 acatccaaga tcaagccaag cacatgggg tgatggcagg cgacatctac tcagtgttcc 1140
 107 gcaatgctgc ctcctttaaa gaagtgtctg acagcctct cactcttagc aaggggcagc 1200
 108 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcctgttaac aacacgcccc 1260
 109 tcaactggct ggttagtccc ttttattcctc agctgactga gtctcagaat gctcaggacc 1320
 110 aaggtgcaga gatggacaag agcagccagg agacccagcg atctgagcat aaaactcatt 1380
 111 aaacctgccc ctatcaactag tgcatgctgt ggccagacag atgacacett ttgttatgtt 1440
 112 gaaattaact tgctaggcaa ccctaaattt ggaagcaagt agctagtata aaggccctca 1500
 113 attgttagtt tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
 114 ctgttcacct ggtaagaaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
 115 aaaattcaaa tgcactttagt ttctcattct atggccatgt tggtgcctct gttactgttt 1680
 116 gtattgaata aaaacatctt catgtggct gggtagaaa ctgggtctg ctctgggttg 1740
 117 atctgaaaag gcgtcttcac tgcttatct catgatgctt gcttgaaaaa cttgatttt 1800
 118 gttttcatt tctcaaataag gaatactacc tttgaattca ataaaattca ctgcaggata 1860
 119 gaccagttna qmagcaaaaca nncaatataca qmnaaganac 1900

W--> 120 <210> SEQ ID NO 5

121 <211> LENGTH: 437

122 <212> TYPE: PRT

123 <213> ORGANISM: Human

124 <400> SEQUENCE: 5

Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
 1 5 10 15
 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
 20 25 30
 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
 35 40 45
 Met (Xaa) Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
 50 55 60
 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
 65 70 75 80
 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
 85 90 95
 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
 100 105 110
 Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp
 115 120 125
 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
 130 135 140
 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
 145 150 155 160

See item 10 on Euro Summary Sheet

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RAW SEQUENCE LISTING
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Input Set: I201916.RAW

145 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
 146 165 170 175
 147 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
 148 180 185 190
 149 Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
 150 195 200 205
 151 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
 152 210 215 220
 153 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
 154 225 230 235 240
 155 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
 156 245 250 255
 157 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
 158 260 265 270
 159 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
 160 275 280 285
 161 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
 162 290 295 300
 163 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
 164 305 310 315 320
 165 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
 166 325 330 335
 167 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
 168 340 345 350
 169 Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
 170 355 360 365
 171 Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
 172 370 375 380
 173 Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
 174 385 390 395 400
 175 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
 176 405 410 415
 177 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
 178 420 425 430
 179 Glu His Lys Thr His
 180 435
 181 <210> SEQ ID NO 6
 182 <211> LENGTH: 31
 183 <212> TYPE: PRT
 184 <213> ORGANISM: Artificial Sequence
 185 <220> FEATURE:
 186 <223> OTHER INFORMATION: A branched peptide containing residues 5-27 of the
 187 HCV core protein with degeneracy at positions 1
 188 and 12 in which position 1 can be Ala or Pro and
 189 position 12 can be Ile or Asn. *use Xaa and explain
in 2207-2237 section*
 190 <400> SEQUENCE: 6
 191 Ala Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile Arg Arg Pro Gln
 192 1 5 10 15
 193 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
 194 20 25 30

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/201,916DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

195 <210> SEQ ID NO 7
196 <211> LENGTH: 11
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
201 protein deletion plasmids.
202 <400> SEQUENCE: 7
203 gctgagatct a 11
204 <210> SEQ ID NO 8
205 <211> LENGTH: 29
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
210 protein deletion plasmids.
211 <400> SEQUENCE: 8
212 gtaaccttcc tggttgctct tgagatcta 29
213 <210> SEQ ID NO 9
214 <211> LENGTH: 17
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
219 protein deletion plasmids.
220 <400> SEQUENCE: 9
221 gtaaccttgc agatcta 17
222 <210> SEQ ID NO 10
223 <211> LENGTH: 18
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
228 protein deletion plasmids.
229 <400> SEQUENCE: 10
230 ctggcgcatg gagatcta 18
231 <210> SEQ ID NO 11
232 <211> LENGTH: 28
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
237 protein deletion plasmids.
238 <400> SEQUENCE: 11
239 ctggcccatg gtgttaacta tgcaacag 28
240 <210> SEQ ID NO 12
241 <211> LENGTH: 31
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:

Input Set: I201916.RAW

Line	?	Error/Warning	Original Text
95	W	"N" or "Xaa" used: Feature required	ctgtgacgac tactgtgact ggggccaagg attctgtn
119	W	"N" or "Xaa" used: Feature required	gaccagttta gnagcaaaca nncangtaca cnnaagan
131	W	"N" or "Xaa" used: Feature required	Met Xaa Glu Asn Gly Val Lys Thr Ile Thr S